



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/828,985A

DATE: 08/30/2004

TIME: 14:44:14

Input Set : A:\RS0210Y.txt

Output Set: N:\CRF4\08302004\J828985A.raw

3 <110> APPLICANT: Armour, Christopher D  
 4 Castle, John C  
 5 Garrett-Engеле, Philip W  
 6 Kan, Zhengyan  
 7 Loerch, Patrick M  
 8 Tsinoremas, Nicholas F  
 10 <120> TITLE OF INVENTION: Novel Isoforms of Centromere Protein E (CENPE)  
 13 <130> FILE REFERENCE: RS0210Y  
 15 <140> CURRENT APPLICATION NUMBER: US 10/828,985A  
 16 <141> CURRENT FILING DATE: 2004-04-21  
 18 <150> PRIOR APPLICATION NUMBER: US 60/464,905  
 19 <151> PRIOR FILING DATE: 2003-04-23  
 21 <150> PRIOR APPLICATION NUMBER: US 60/510,701  
 22 <151> PRIOR FILING DATE: 2003-10-10  
 24 <160> NUMBER OF SEQ ID NOS: 25  
 26 <170> SOFTWARE: PatentIn version 3.2  
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 29 <211> LENGTH: 40  
 30 <212> TYPE: DNA  
 31 <213> ORGANISM: Homo sapiens  
 33 <400> SEQUENCE: 1  
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 67 <212> TYPE: DNA

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 82 gaatcacttg gagaaaactgc ccaagtttac tggaaaactg acaaataatgt catttatcaa 120  
 84 gttgatggaa gtaaatcctt caattttgat cgtgtcttc atggtaatga aactaccaaa 180  
 86 aatgtgtatg aagaatagc agcaccaatc atcgattctg ccatacacaagg ctacaatgg 240  
 88 actatatttg cctatggaca gactgcttca ggaaaaacat ataccatgat gggttcagaa 300  
 90 gatcatttgg gagttatacc caggcaatt catgacattt tccaaaaaaaaat taagaagtt 360  
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 104 agagctgctc aaacaggcgc tgcaagggtgt cggtctcaagg aaggctgtaa tataaatcga 780  
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 128 gagatagaat ggaatccacg aacaaagcta ctaaatcagg agaatataga aagttagttg 1500  
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 138 gtagagctgc tttagaaaaaa ggaagagaccag attaagaagc tacaggaata catagactct 1800  
 140 caaaaagctag aaaatataaa aatggacttg tcataactcat tggaaagcat tgaagaccca 1860  
 142 aaacaaatga agcagactct gttgatgtt gaaactgtat cccttgatgc caagagagaa 1920  
 144 tcagcccttc tttagaagtga aaatctggag ttgaaggaga aaatgaaaga acttgcaact 1980  
 146 acatacaago aaatggaaaa tgatattcag ttatataaaa gccaattggg ggcaaaaaaaag 2040  
 148 aaaatgcaag ttgatctggaa gaaagaatttta caatctgtt ttaatgagat aacaaaactc 2100  
 150 acctccctta tagatggcaaa agttccaaaaa gatttgcattt gtaatttggg attggaaagg 2160  
 152 aagattactg atcttcagaa agaactaaat aaagaatgtt aagaaaaatgaa agcttgcgg 2220  
 154 gaagaagtca ttttgcatttca agaattgaaa tctttacattt ctgaagttaga aaggctgagg 2280  
 156 aaagagatac aagacaaatc tgaagagctc catataataa catcagaaaaa agataaaatgg 2340  
 158 tttctgttca agttcataa ggagagtttca gttcaaggat ttttgcattt aattggaaaa 2400  
 160 acaaaaqatq acctaqaac tacacagtcg aattataaaa qcactgtatca aqaaattccaa 2460

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164	gagagaatga atcaggaaat	tgattcgagt	2580
166	ttgggtgtt tgaagaccga	cccäääatt	2640
168	gagggtcaag aaagactaaa	cagctgaagg	2700
170	tctccgctgc aaactgttaga	aacaatttaga	2760
172	ttagaagaag taaaactt	aaagatgatc	2820
174	ttgcaaattt agagggacca	actcaaaagt	2880
176	gatactcaag aacaattacg	aatgcctt	2940
178	aatacactaa aatcgaaaat	ttctgaggaa	3000
180	acaggagaaa ctaaagatga	atttcagcaa	3060
182	ttggaaagcta aaaataccca	aacactaact	3120
184	caacaaagga agatattttc	ttaatacag	3180
186	agtgttatag cagaaaagga	acaattgaag	3240
188	attgaaaacc aggaagaatt	aagacttctt	3300
190	gttgcacaag aaaagaacca	tgccataaaag	3360
192	agactggcag aagttgaaga	aaaactaaag	3420
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198	aggcttgagt tggctcagaa	acttaatgaa	3600
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202	ggatatataa gagaatttga	agctacaggc	3720
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212	acaacactgg caagaataga	aatggaaagg	4020
214	caggaagaga taaaatctct	aaccaaggaa	4080
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220	aaaatcgta gtgagatgga	gcaattcaaa	4260
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224	gctaaggaga aagatgacct	acagaggctg	4380
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228	gttgctcatt gttgcctgaa	agaacaagag	4500
230	tcagagaagg aaactgaaat	atcaaccatt	4560
232	ttacagaaca agatccaaga	gatttatgag	4620
234	agtggatc aggaaaacgt	gaatgaactg	4680
236	gattcagcac tacaaggat	agaaagtaag	4740
238	agtcaagaag aaatacaaat	tatgattaag	4800
240	gcccttcaga tagagagaga	ccaaactgaaa	4860
242	aaagaatctc aaaaaaaa	atatcagttt	4920
244	gagaaaatgt gtgaaataga	acacttgaag	4980
246	gaaaacatag aaacggagaa	tataaggtt	5040
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254	agagggattt ttcagagaa	aacaaatgaa	5280
256	tcaaataatgtg cctaaaagc	acaggatctg	5340
258	atgcataatgtg aagagcagca	ggaaacttatt	5400

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262	aagattcaag aacttaaggc aaatgaacat caacttatta cgttaaaaaa agatgtcaat	5520
264	gagacacaga aaaaagtgtc tgaaatggag caactaaaga aacaataaaa agaccaaagc	5580
266	ttaactctga gtaaaatttga aatagagaat ttaaatttgg ctcaagaact tcataaaaaac	5640
268	cttgaagaaa tgaaatctgt aatgaaagaa agagataatc taagaagagt agaggagaca	5700
270	ctcaaactgg agagagacca actcaaggaa agcctgcaag aaaccaaagc tagagatctg	5760
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274	gataaactta gagaaaaaat ttcagaaaag acaattcaaa ttccagacat tcaaaaggat	5880
276	ttagataaat caaaagatga attacagaaa aaggaccgac agaaccacca agtaaaacct	5940
278	gaaaaaaaggt tactaagtga tggacaacag caccttatgg aaagcctgag agaaaagtgc	6000
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282	aatagattgt ctcttgactt ggagaaggaa attgaattcc acagaatcat gaagaaactg	6120
284	aagtatgtgt taagctatgt tacaaaaata aaagaagaac aacatgaatg catcaataaa	6180
286	tttggaaatgg attttattga tgaagtggaa aagcaaaaagg aattgctaatt taaaatacacag	6240
288	caccccaac aagattgtga tgtaccatcc agagaattaa gggatctcaa attgaaccag	6300
290	aatatggatc tacatattga gggaaatttcc aaagatttct cagaaagtga gttccctagc	6360
292	ataaagactg aatttcaaca agtactaagt aataggaaag aaatgacaca gttttggaa	6420
294	gagttgttaa atactcggtt tgatatagaa aagcttaaaa atggcatcca gaaagaaaaat	6480
296	gataggattt gtcaagtgaa taacttctt aataacagaa taattgcatt aatgaatgaa	6540
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302	gcattttttt cccaggtaa tcctaccaca caagacaata agaatccca tggatccatca	6720
304	agagctacac agttaaccac agagaaaaattt cgagagctgg aaaatttcaact gcatgaagct	6780
306	aaagaaaatg ctatgcataa gggaaagcaag attataaaga tgcagaaaga acttgagggt	6840
308	actaatgaca taatagcaaa acttcaagcc aaagttcatg aatcaaataa atgccttgaa	6900
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322	aaagaaaattt ctaagttaaa gcagaaaaat gaacagctaa taaaacaaaaa gaatgaattt	7320
324	ttaagcaata atcagcatct ttccatgtt gtc当地actt ggaaggaaag aacccttaaa	7380
326	agagaggctc acaaacaatg aactttagttag aatttccaa agtctccaa agtactgga	7440
328	acagcttctt aaaaagaaaca aattacaccc tctcaatgca aggaacgaa tttacaagat	7500
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332	tcacccatc cagttcgctt ttttataac tcaagtttag gcctttgtcc agaggtgaa	7620
334	aatgc当地 cagagagtgt ggattcttag ccaggtcctt ggcacgcctc ctcaggcaag	7680
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339 &lt;210&gt; SEQ ID NO: 7

340 &lt;211&gt; LENGTH: 2568

341 &lt;212&gt; TYPE: PRT

342 &lt;213&gt; ORGANISM: Homo sapiens

344 &lt;400&gt; SEQUENCE: 7

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347 1 5 10 15

350 Asn Ser Arg Glu Glu Ser Leu Gly Glu Thr Ala Gln Val Tyr Trp Lys

351 20 25 30

354 Thr Asp Asn Asn Val Ile Tyr Gln Val Asp Gly Ser Lys Ser Phe Asn

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362	Glu Ile Ala Ala Pro Ile Ile Asp Ser Ala Ile Gln Gly Tyr Asn Gly			
363	65	70	75	80
366	Thr Ile Phe Ala Tyr Gly Gln Thr Ala Ser Gly Lys Thr Tyr Thr Met			
367	85	90	95	
370	Met Gly Ser Glu Asp His Leu Gly Val Ile Pro Arg Ala Ile His Asp			
371	100	105	110	
374	Ile Phe Gln Lys Ile Lys Lys Phe Pro Asp Arg Glu Phe Leu Leu Arg			
375	115	120	125	
378	Val Ser Tyr Met Glu Ile Tyr Asn Glu Thr Ile Thr Asp Leu Leu Cys			
379	130	135	140	
382	Gly Thr Gln Lys Met Lys Pro Leu Ile Ile Arg Glu Asp Val Asn Arg			
383	145	150	155	160
386	Asn Val Tyr Val Ala Asp Leu Thr Glu Glu Val Val Tyr Thr Ser Glu			
387	165	170	175	
390	Met Ala Leu Lys Trp Ile Thr Lys Gly Glu Lys Ser Arg His Tyr Gly			
391	180	185	190	
394	Glu Thr Lys Met Asn Gln Arg Ser Ser Arg Ser His Thr Ile Phe Arg			
395	195	200	205	
398	Met Ile Leu Glu Ser Arg Glu Lys Gly Glu Pro Ser Asn Cys Glu Gly			
399	210	215	220	
402	Ser Val Lys Val Ser His Leu Asn Leu Val Asp Leu Ala Gly Ser Glu			
403	225	230	235	240
406	Arg Ala Ala Gln Thr Gly Ala Ala Gly Val Arg Leu Lys Glu Gly Cys			
407	245	250	255	
410	Asn Ile Asn Arg Ser Leu Phe Ile Leu Gly Gln Val Ile Lys Lys Leu			
411	260	265	270	
414	Ser Asp Gly Gln Val Gly Gly Phe Ile Asn Tyr Arg Asp Ser Lys Leu			
415	275	280	285	
418	Thr Arg Ile Leu Gln Asn Ser Leu Gly Gly Asn Ala Lys Thr Arg Ile			
419	290	295	300	
423	Ile Cys Thr Ile Thr Pro Val Ser Phe Asp Glu Thr Leu Thr Ala Leu			
424	305	310	315	320
427	Gln Phe Ala Ser Thr Ala Lys Tyr Met Lys Asn Thr Pro Tyr Val Asn			
428	325	330	335	
431	Glu Val Ser Thr Asp Glu Ala Leu Leu Lys Arg Tyr Arg Lys Glu Ile			
432	340	345	350	
435	Met Asp Leu Lys Lys Gln Leu Glu Glu Val Ser Leu Glu Thr Arg Ala			
436	355	360	365	
439	Gln Ala Met Glu Lys Asp Gln Leu Ala Gln Leu Leu Glu Glu Lys Asp			
440	370	375	380	
443	Leu Leu Gln Lys Val Gln Asn Glu Lys Ile Glu Asn Leu Thr Arg Met			
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**VERIFICATION SUMMARY**

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